AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application.

LISTING OF CLAIMS:

Claim 1 (Currently Amended): A diagnostic method for detecting and identifying bacterial species causing infections from a clinical sample, comprising

a) amplifying DNA isolated from said clinical sample using a mixture of DNA primers comprising sequences which hybridize with conserved regions of genes encoding topoisomerases of infectious bacterial species, said DNA primers comprising the sequences of SEQ ID NO: 76 and 77 or complementary sequences thereof ~~or functional fragments thereof~~,

b) contacting the amplified DNA with a combination of oligonucleotide probes that hybridize under normal hybridization conditions with hyper-variable regions situated near said conserved regions of genes encoding topoisomerases of infectious bacterial species, said probes being bacterial species-specific under said hybridization conditions, and

c) detecting the formation of a hybridization complex and identifying said infectious bacterial species based on said detection.

Claim 2 (Previously Presented): The diagnostic method according to claim 1, wherein said topoisomerase is selected from *gyrB* and *parE* and said infectious bacterial species are bacterial species that cause respiratory tract infections.

Claim 3 (Previously Presented): The diagnostic method according to claim 1, wherein said hyper-variable region is the hyper-variable region of the gene encoding the *gyrB* and/or *parE* protein of a bacterial species selected from *Streptococcus pneumoniae, Streptococcus pyogenes, Chlamydia pneumoniae, M ycoplasma pneumoniae, Haemophilus influenzae, Staphylococcus aureus, Pseudomonas aeruginosa, Neisseria gonorrhoeae, Escherichia coli, Moraxella catarrhalis, Legionella pneumophila*, and *Fusobacterium necropho rum*.

Claim 4 (Previously Presented): The diagnostic method according to claim 1, wherein the length of oligonucleotide probe sequences used in step b) is 15 - 30 nucleic acids.

Claim 5 (Currently Amended): The diagnostic method according to claim 1, wherein said combination of oligonucleotide probes comprises all or a portion of the sequences identified with SEQ ID NO: 1 to 69, and/or complementary sequences thereof~~, or functional fragments thereof~~.

Claim 6 (Previously Presented): The diagnostic method according to claim 5, wherein said combination of oligonucleotide probes comprises all the sequences identified with SEQ ID NO: 1 to 69.

Claim 7 (Previously Presented): The diagnostic method according to claim 1, wherein said combination of oligonucleotide probes is attached to a solid support.

Claim 8 (Previously Presented): The diagnostic method according to claim 1, wherein the DNA amplified from the clinical sample in step a) is amplified using the polymerase chain reaction (PCR) and that the DNA contacted in step b) is contacted with bacterial species-specific oligonucleotide probes attached onto a solid support.

Claim 9 (Previously Presented): The diagnostic method according to claim 7, wherein said solid support is treated glass.

Claim 10 (Previously Presented): The diagnostic method according to claim 1, wherein suitably labeled nucleotides are used in the amplification of DNA isolated from a clinical sample in step a) to generate a detectable target strand.

Claim 11 (Previously Presented): The diagnostic method according to claim 9, wherein the amplified and optionally labeled target DNA in step b) is contacted with a solid support, on which all bacterial species-specific oligonucleotide probes identified with SEQ ID NO: 1 to 69 and/or complementary sequences thereof have been attached.

Claim 12 (Previously Presented): The diagnostic method according to claim 11, wherein the amplified and optionally labeled target DNA in step b) is contacted with a solid support on which specific oligonucleotide probe sequences detecting one specified bacterial species or a few specified bacterial species causing infections have been attached, said sequences being selected from sequences shown in Tables 4A and 4B and/or complementary sequences thereof.

Claim 13 (Previously Presented): The diagnostic method according to claim 1, wherein microarray technology is used in step c).

Claim 14 (Currently Amended): A DNA primer mixture comprising sequences that hybridize with sequences of the conserved regions of genes encoding topoisomerases of bacterial species that cause infections, said mixture comprising sequences identified with SEQ ID NO: 76 and 77 and/or reversed or complementary sequences thereof ~~or functional fragments thereof~~.

Claim 15 (Currently Amended): An oligonucleotide probe sequence useful in the diagnosis of infection causing bacterial species, wherein said oligonucleotide probe sequence hybridizes under normal hybridization conditions with a sequence of a hyper-variable region that can be amplified by primer sequences identified with SEQ ID NO: 76 and 77 and/or reversed or complementary sequences thereof ~~or functional fragments thereof~~, that is bacterial species-specific, and that is situated near the conserved regions of genes encoding topoisomerases, said oligonucleotide probe sequence being one of the sequences identified with SEQ ID NO: 1 to 69 and/or complementary sequences thereof ~~or functional fragments thereof~~.

Claims 16-18 (Canceled).

Claim 19 (Currently Amended): A diagnostic kit for use in the diagnosis of infection-causing bacteria comprising

a) a DNA primer mixture comprising sequences that hybridize with conserved regions of genes encoding topoisomerases of infectious bacterial species, said mixture comprising the sequences identified with SEQ ID NO: 76 and 77 and/or complementary sequences thereof ~~or functional fragments thereof~~

b) a combination of bacterial species-specific oligonucleotide probes comprising any combination of the sequences identified with . SEQ ID NO: 1 to 69 and/or complementary sequences thereof ~~or functional fragments thereof~~,

c) positive and optionally negative control probe sequences, and optionally

d) reagents required in the amplification, hybridization, purification washing, and/or detection steps.

Claim 20 (Previously Presented): A diagnostic kit of claim 19, wherein said topoisomerases are selected from the *gyrB* and/or *parE* proteins of bacterial species that cause respiratory tract infections.

Claim 21 (Previously Presented): A diagnostic kit of claim 20, wherein said combination of oligonucleotide probe sequences is attached onto a solid support.

Claim 22 (Previously Presented): The DNA primer mixture of claim 14, wherein said topoisomerases are selected from the *gyrB* and/or *parE* proteins of bacterial species that cause respiratory tract infections.

Claim 23 (Previously Presented): The diagnostic method according to claim 1, wherein the length of oligonucleotide probe sequences used in step b) is 20 – 30 nucleic acids.

Claim 24 (Previously Presented): The diagnostic method according to claim 1, wherein the length of oligonucleotide probe sequences used in step b) is 21 – 25 nucleic acids.